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1	CTMS	1

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US-09-544-517-1

AA174423

LOCUS

ACCESSION AA174423

ACCESSION AA174423

VERSION AA174423.1 GI:1755545

KEYWORDS EST.

SOURCE house mouse.

ORGANISM	Mus musculus
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Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 587)

AUTHORS

1 (bases 1 to 587)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE

JOURNAL Unpublished (1996)

COMMENT

Unpublished (1998)  
Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:377585

MGI:377585  
Possible reversed clone: similarity on wrong strand

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 335.

## FEATURES

source

Location/Qualifiers

1. .587

```
/organism="Mus musculus"
```

```
/strain="C57BL/6J"
```

```
/db xref="taxon:10090"
```

```
/clone="IMAGE:616761"
```

```
/clone lib="Soares mouse 3NbMS"
```

```
/clone_lib=  
/sex="male"
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```
/sex= male
/tissue type="Spleen"
```

```
/dev stage="4 weeks"
```

```
/lab_host="DH10B"
```

```

/lab_host= DR10B
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
primed with 5' Not I - oligo(dT) primer [5'

```

was primed with a Not I - oligo(dT) primer (5'-TGTTACCAATCTGAAGTGGGAGCGCCGCGCTGTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through

three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT

138 a      123 c      148 g      178 t

ORIGIN

```

Query Match          35.1%;  Score 382;  DB 9;  Length 587;
Best Local Similarity 86.5%;  Pred. No. 2.5e-76;
Matches 434;  Conservative 0;  Mismatches 65;  Indels 3;  Gaps 1;

```

[illegible]

Qy 214 agcattctcccggaataatctcaggaagcaatgcaccagggtgacaacgctaactggaaa 273  
|||||

Db 149 AGCATTCTCCCGGATAATCTCAGGAAGCAGTGCACCAGGGTGACCACGCTAACTGGAAA 208

Qy 274 gaaaattatagaaacatggaaagatgccagaattcatgttggtggaagaagtagagccgag 333  
||||| ||||||| ||| ||||||| | ||||||| || || ||||||| ||

Db 209 GAAACTTATAGAAACCTGGGAAGATGCCACAGTTCATGTTGTG---GAGACAGAGCCCAG 265

Qy 334 cagtgggggtggttggttatgtgcaggaccttagctcggacctgcaagttggcgttat 393  
| ||||||| ||||||| ||||||| || ||||||| || ||||||| ||

Db 266 CGGTGGGGGTGGTTGTGGCTATGTGCAGGACCTTACCTTGGACCTGCAAGTTGGCGTTAT 325

Qy 394 taagccatggttgctcctaggtcacaagatgctgctcatgatttggatacactgaaaaa 453  
||||| ||||||| || ||||||| ||||||| ||||||| || || ||||||| ||

Db 326 TAAGCCCTGGTTGCTTCTGGGGTCACAGGATGCTGCTCATGACCTGGAGCTACTGAGAAA 385

Qy 454 gaataaggtgactcatattcttaatgttgcatatggagttgaaaatgctttcctcagtga 513  
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Db 386 GCATAAGGTGACTCATATTCTCAATGTTGCATATGGAGTTGAAAATGCTTTCCTCAGTGA 445

Qy 514 ctttacatataagagcatttctatattggatctgcctgaaaccaacatcctgtcttattt 573  
||||| ||||||| ||||||| || ||||||| ||||||| ||||||| ||||||| ||

Db 446 GTTTACATATAAGACCATTTCTATACTGGATGTGCCTGAAACCAATATCCTGTCTTATTT 505

Qy 574 tccagaatgttttgaattttattgaagaagcaaaaagaaaagatggagtggttcttgttca 633  
||||| ||||||| ||||||| || || || || || || || || || || || || ||

Db 506 TCCAGAATGTTTGTAGTTTATTGAGCAAGCCAACTGAAGGATGGCGTGGTTCTCGTGCA 565

Qy 634 ttgtaatgcaggcggtttccagg 655  
||||| |||||||

Db 566 CTGTAATGCAGGTGTTTCCAGG 587



Accession	Position	Sequence	Length
Db	151	AGCATTCTCCCGGGATAATCTCAGGAAGCAGTGCACCAGGGTGACCACGCTAACTGGA	210
Qy	274	gaaaattatagaacatggaaagatgccagaattcatgttgtggaagaagtagagccgag	333
Db	211	GAAACTTATAGAAACCTGGGAAGATGCCACAGTTCATGTTGTGGAGACAG--AGCCCAGC	268
Qy	334	cagtgggggtggttgtggttatgtgcaggaccttagctcggacctgcaagttggcggttat	393
Db	269	GATGGGTGGTGGTTGTGGCTATGTGCAGGACCTTACCTTGGACCTGCAAGTTGGCGTTAT	328
Qy	394	taagccatggttgctcctagggtcacaagatgctgctcatgatttggatacactgaaaaa	453
Db	329	TAAGCCCTGGTTGCTTCTGGGGTCACAGGATGCTGCTCATGACCTGGAGCTACTGAGAAA	388
Qy	454	gaataaggtgactcatattcctaattgttgcataatggagttgaaaatgctttcctcagtga	513
Db	389	GCATAAGGTGACTCATATTCTCAATGTTGCATATGGAGTTGAAAATGCTTTCCTCAGTGA	448
Qy	514	ctttacatataagagcatttctatattggatctgcctgaaaccaacatcctgtcttattt	573
Db	449	GTTTACATATAAGACCATTCTATACTGGATGTGCCTGAAACCAATATCCTGTCTTATTT	508
Qy	574	tccagaatgttttgaatttattgaagaagcaaaaagaaaagatggagtggttcttgttca	633
Db	509	TCCAGAATGTTTTGAGTTTATTGAGCAAGCAGAACTGAAGGATGGCGTGGTTCTCGTGCC	568
Qy	634	ttgtaatgcaggcgtttccagggctgctgcaattgtaataggtttctgatgaattctga	693
Db	569	CTGTTATGCAGGTGTTTCCAGGGCTGCTGCAGTTGTACTTGGGCTTCCCCTGAGTTCTGA	628
Qy	694	acaaacctcatttaccagtgccttttctttggtgaaaaatgcaagaccttccatattgtcc	753
Db	629	GGAAGCCCCTTTCACCCCTGCCCTGTCGTTGGTGGGAAGAGGGCGGGACTTCCTTATGTCC	688
Qy	754	aa 755	
Db	689	GA 690	

Title: US-09-544-517-1

RESULT 6

AI033989/c

LOCUS

DEFINITION

AI033989 486 bp mRNA linear EST 27-AUG-1998  
ow13b01.x1 Soares\_parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone  
IMAGE:1646665 3' similar to TR:P78512 P78512 DUAL SPECIFICITY  
PROTEIN PHOSPHATASE HOMOLOG HMKP-R ;, mRNA sequence.

ACCESSION

AI033989

VERSION

AI033989.1 GI:3254942

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 486)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo,  
Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 703 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 293.

FEATURES

source

Location/Qualifiers

1. .486

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1646665"

/clone\_lib="Soares\_parathyroid\_tumor\_NbHPA"

/tissue\_type="parathyroid tumor"

/dev\_stage="adult"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia)  
) with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT  
TTTTT-3'], double-stranded cDNA was size selected, ligated  
to Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pT7T3  
vector (Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid  
adenomas was kindly provided by Dr. Stephen Marx, National  
Institute of Diabetes and Digestive and Kidney Diseases,  
NIH."

BASE COUNT

164 a 95 c 80 g 147 t

ORIGIN

Query Match 42.7%; Score 463.8; DB 9; Length 486;

Best Local Similarity 98.4%; Pred. No. 7.1e-95;

Matches 479; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy 596 gaagaagcaaaaagaaaagatggagtggttcttggttcattgtaatgcaggcggtttccagg 655  
|||||

Db 486 GAAGAAGCAAAAAGAAAAGATGGAGTGGTTCTTGTTTCATTGT-ATGCAAGCGTTTCCAGG 428

Qy 656 gctgctgcaattgtaataggtttcctgatgaattctgaacaaacctcatttaccagtgct 715  
|||||

Db 427 GCTGTTGCAATTGTAATAGGTTTCTGATGAATTCTGAACAAACCTCATTACCAGTGCT 368

Qy 16 ttttctttggtgaaaaatgcaagaccttccatatgtccaaattctggcttcatggagcag 775  
 |||||  
 Db 367 TTTTCTTTGGTGAAAAATGCAAGACCTTCCATATGTCCAAATTCTGGCTTCATGGAGCAG 308  
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 Qy 776 cttcgtacatatcaagagggcaaagaaagcaataagtgtgacagaatacaggagaaacagt 835  
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 Db 307 CTTCGTACATATCAAGAGGGCAAAGAAAGCAATAAGTGTGACAGAATACAGGAGAACAGT 248  
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 Qy 836 tcatgagttgcattgtagcagacaatggacaactgtagtttctgaattgacttctatagc 895  
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 Db 247 TCATGAGTTGCATTGTAGCAGACAATGGACAACGTAGTTTCTGAATTGACTTCTATAGC 188  
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 Qy 896 catcttttcccttttttggagagtagactagcaaaactcccttttttctcttgccctttt 955  
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 Db 187 CATCTTTTCCCTTTTTTGGAGAGTAGACTAGCAAAATTCCCTTTTTTCTCTTGCCTTTTT 128  
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 Qy 956 tatgcataaatggaggtcaatctgattgtcctgacctactgtataagtaaatttcaaagt 1015  
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 Db 127 TATGCATAAATGGAGGTCAATTTGATTGTCCTGACCTACTGTATAAGTAAATTTCAAATG 68  
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 Qy 1016 tcattactttctctttgttattataatgtgtgattaaatgcttttttaaattgctaaggg 1075  
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 Db 67 TCATTACTTTCTCTTTGTTATTATAATGTGTGATTAAATGCTCCTTTAAATTGCTAAGGG 8  
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 Qy 1076 aaaataa 1082  
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 Db 7 AAAAAA 1

